

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

IN RE APPLICATION OF: Lynn Stam

U.S. APPLICATION NO.: 10/527,571

INTERNATIONAL APPLICATION NO: PCT/US2003/024982

INTERNATIONAL FILING DATE: 08 August 2003

TITLE: NUCLEIC ACID SEQUENCES FROM DROSOPHILA  
MELANOGASTER THAT ENCODE PROTEINS ESSENTIAL FOR  
VIABILITY AND USES THEREOF

Mail Stop PCT  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450


**SUBMISSION OF SUBSTITUTE SEQUENCE LISTING  
INCLUDING STATEMENT OF VERIFICATION**

Sir:

Applicants hereby submit three copies of the Computer Readable Form of the Substitute Sequence Listing on CD-R. The undersigned states that the three compact discs, submitted in accordance with 37 CFR § 1.821 (c) and (e), and 1.52(e), respectively, are the same.

Respectfully submitted,

Syngenta Biotechnology, Inc.  
Patent Department  
P.O. Box 12257  
Research Triangle Park, NC 27709-2257

  
Mary Kakefuda  
Attorney for Applicants  
Reg. No. 39,245  
Phone: (919) 765-5071

Date: March 17, 2006

#8

**STIC Biotechnology Systems Branch****RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/527,571  
Source: PGT  
Date Processed by STIC: 01/31/2006

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
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Revised 01/24/05



PCT

## RAW SEQUENCE LISTING

DATE: 01/31/2006

PATENT APPLICATION: US/10/527,571

TIME: 15:59:57

Input Set : N:\SMITH\PTO.TS.txt

Output Set: N:\CRF4\01312006\J527571.raw

3 <110> APPLICANT: Syngenta Participations AG  
 4 Stam, Lynn  
 5 Kamdar, Kim  
 6 Spana, Eric  
 7 Bachmann, Jane  
 9 <120> TITLE OF INVENTION: Nucleic Acid Sequences from Drosophila Melanogaster that  
 10 Encode Proteins Essential for Viability and Uses Thereof  
 12 <130> FILE REFERENCE: 70131WOPCT  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/527,571  
 C--> 15 <141> CURRENT FILING DATE: 2005-03-14  
 17 <150> PRIOR APPLICATION NUMBER: 60/422,377  
 18 <151> PRIOR FILING DATE: 2002-10-29  
 20 <160> NUMBER OF SEQ ID NOS: 381  
 22 <170> SOFTWARE: PatentIn version 3.1

Does Not Comply  
 Corrected Diskette Needed  
 CPR-4,5,6

## ERRORED SEQUENCES

7736 <210> SEQ ID NO: 61  
 7737 <211> LENGTH: 1022  
 7738 <212> TYPE: PRT  
 7739 <213> ORGANISM: Drosophila melanogaster  
 7741 <400> SEQUENCE: 61  
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 7744 1 5 10 15  
 7747 Asp Gly Ser Pro Pro Val Lys Lys Leu Arg Leu Gln Thr Leu Ala Ala  
 7748 20 25 30  
 7751 Asp Ala Lys Gly Gly Lys Ser Gly Lys Val Gly Asn Val Glu Arg Lys  
 7752 35 40 45  
 7755 Leu Thr Ala Leu Asn Gln Leu Asp Ala Tyr Val Gly Asn Leu Pro Ala  
 7756 50 55 60  
 7759 Gly Ala Leu Val Leu Pro Thr Gly Thr Pro Val Ala Ser Thr Gly Ala  
 7760 65 70 75 80  
 7763 Pro Ser Thr Gly Val Ile Gly Asn Pro Pro Ala Ala Ala Thr Gly Ala  
 7764 85 90 95  
 7767 Pro Pro Met Thr Ala Ala Asn Ser Arg Glu Leu Leu Glu Leu Val  
 7768 100 105 110  
 7771 Lys Ile Thr Asp Glu Ile Ser Tyr Glu Asp Val Glu Met Gly Glu Leu  
 7772 115 120 125  
 7775 Lys Glu Val Ala Ser Lys Ile Phe Gln Leu Tyr Gln Leu Gln Glu Arg  
 7776 130 135 140  
 7779 Asp Ser Asp Thr Ser Ile Arg Val Lys Leu Leu Glu Leu Leu Ser Gly  
 7780 145 150 155 160

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Input Set : N:\SMITH\PTO.TS.txt

Output Set: N:\CRF4\01312006\J527571.raw

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7783 Leu Gly Cys Glu Cys Ala Thr Glu Gln Ala Leu Thr Met Ile Ile Asp
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7787 Tyr Phe Ile Phe Leu Leu Arg Lys Glu Val Ser Gln Lys Val Leu Ala
7788                      180                      185                      190
7791 Gln Gly Met Met Cys Leu Phe Arg Ile Gly Glu Arg Arg Lys His Met
7792                      195                      200                      205
7795 Leu Pro Ile Ser Tyr Lys Thr Gln Val Ala His Leu Ala Lys Glu Gln
7796                      210                      215                      220
7799 Leu Arg Ser Gly Ser Ala His Thr Gln Lys Asn Ala Met Leu Val Ile
7800 225                      230                      235                      240
7803 Gly Arg Phe Ala Thr Lys Met Glu Gly Glu Arg His Tyr Val Trp Lys
7804                      245                      250                      255
7807 Leu Ala Phe Tyr Ile Asp Ser Gln Asp Ser Ser Val Arg Ala Gln Ala
7808                      260                      265                      270
7811 Leu His Ala Leu Leu Thr Leu Gly Glu Arg Gly Ser Gln Leu Pro Ala
7812                      275                      280                      285
7815 Val Leu Tyr Lys Arg Ala Val Glu Ala Met Lys Asp Asp Tyr Glu Cys
7816                      290                      295                      300
7819 Val Arg Lys Glu Ala Leu Gln Leu Val Phe Met Leu Gly Asn Arg His
7820 305                      310                      315                      320
7823 Pro Asp Tyr Ile Leu Pro Ser Asp Arg Gln Gln Glu Glu Leu Arg Met
7824                      325                      330                      335
7827 Ile Asp Ala Ala Phe Ser Lys Val Cys Glu Ala Leu Cys Asp Leu Ser
7828                      340                      345                      350
7831 Leu Gln Ile Arg Val Leu Ala Ala Glu Leu Leu Gly Gly Met Thr Ala
7832                      355                      360                      365
7835 Val Ser Arg Glu Phe Leu His Gln Thr Leu Asp Lys Lys Leu Met Ser
7836                      370                      375                      380
7839 Asn Leu Arg Arg Lys Arg Thr Ala His Glu Arg Gly Ala Arg Leu Val
7840 385                      390                      395                      400
7843 Ala Ser Gly Glu Trp Ser Ser Gly Lys Arg Trp Ala Asp Asp Ala Pro
7844                      405                      410                      415
7847 Gln Glu His Leu Asp Ala Gln Ser Ile Ser Ile Ile Ala Ser Gly Ala
7848                      420                      425                      430
7851 Cys Gly Ala Leu Ile His Gly Leu Glu Asp Glu Phe Leu Glu Val Arg
7852                      435                      440                      445
7855 Thr Ala Ala Val Ala Ser Met Cys Lys Leu Ala Leu Ser Arg Pro Asp
7856                      450                      455                      460
7859 Phe Ala Val Thr Ser Leu Asp Phe Leu Val Asp Met Phe Asn Asp Glu
7860 465                      470                      475                      480
7863 Ile Glu Asp Val Arg Leu Lys Ala Ile Tyr Ser Leu Thr Ala Ile Ala
7864                      485                      490                      495
7867 Lys His Ile Val Leu Arg Glu Asp Gln Leu Glu Ile Met Leu Gly Ser
7868                      500                      505                      510
7871 Leu Glu Asp Tyr Ser Val Asp Val Arg Glu Gly Leu His Leu Met Leu
7872                      515                      520                      525
7875 Gly Ala Cys Arg Val Ser Thr Gln Thr Cys Leu Leu Met Val Val Gln
7876                      530                      535                      540
7879 Lys Leu Leu Asp Val Leu Ala Lys Tyr Pro Gln Asp Arg Asn Ser Thr

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Input Set : N:\SMITH\PTO.TS.txt

Output Set: N:\CRF4\01312006\J527571.raw

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7880 545          550          555          560
7883 Tyr Ala Cys Met Arg Lys Ile Gly Gln Lys His Pro His Leu Val Met
7884          565          570          575
7887 Ala Val Ala Val His Leu Leu Tyr Val His Pro Phe Phe Glu Thr Pro
7888          580          585          590
7891 Glu Arg Asp Val Glu Asp Pro Ala Tyr Leu Cys Val Leu Ile Leu Val
7892          595          600          605
7895 Phe Asn Ala Ala Glu His Leu Val Pro Ile Ile Ser Leu Leu Pro Thr
7896          610          615          620
7899 Ala Thr His Arg His Tyr Ala Tyr Leu Arg Asp Ser Met Pro Asn Leu
7900 625          630          635          640
7903 Val Pro Gln Leu Pro Ile Glu Gly Ala Ser Ser Ala Ser Ala Thr His
7904          645          650          655
7907 Arg Ile Asp Ser Ala Met His Gln Ala Gly Ser Ser Ala Glu Tyr Leu
7908          660          665          670
7911 Gln Met Ile Leu Ser His Ile Glu Glu Ile Phe Thr Met Thr Asp Glu
7912          675          680          685
7915 Arg Leu Glu Leu Leu Gln Thr Ala Gln Ser Asn Leu Gln Arg Leu Gly
7916          690          695          700
7919 Ser Ile Asp Ala Gly Met Tyr Gly Thr Ser Asn Phe Leu Glu Thr Phe
7920 705          710          715          720
7923 Leu Ala Ala Gln Ile Gln Ile Glu Gln Met Gln Arg Cys Ala Ser Thr
7924          725          730          735
7927 Gln Arg Ser Arg Val Pro Leu Lys Glu Ser Leu Ala Ala Leu Ile Arg
7928          740          745          750
7931 Asn Cys Leu Lys Leu Gln His Thr Phe Ser Gly Leu Asn Tyr Gly Asp
7932          755          760          765
7935 Ile Leu Gln Val Lys Gln Leu Arg Leu Arg Ala Cys Ala Leu His Leu
7936          770          775          780
7939 Val Leu Val Val Arg Asp Arg Ser Gln Ser Ala Leu Gly Pro Cys Gln
7940 785          790          795          800
7943 Met Leu Leu Gln Thr Ala Gly Asp Ile Ser Glu Phe Ile Lys Ala Asn
7944          805          810          815
7947 Thr Lys Asp Glu Glu Glu Lys Pro Pro Val Val Glu Thr Asp Met Pro
7948          820          825          830
7951 Met Lys Glu Ser Val Ser Arg Asp Ala Gln Pro Asp Ser Phe Thr Arg
7952          835          840          845
7955 Gln Leu Leu Ile Lys Leu Asp Gly Ile Ser Asp Pro Lys Pro Gly Arg
7956          850          855          860
7959 Val Phe Arg Glu Ile Leu Pro Leu Val Gln Gln Ala Pro Pro Leu Ala
7960 865          870          875          880
7963 Leu Pro Pro Ala Asn Asp Lys Ile Arg Arg Cys Val Ala Asn Ile Leu
7964          885          890          895
7967 Glu Pro Cys Pro Leu Gln Ser Gln Asp Asn Val Ile Lys Val Thr Ala
7968          900          905          910
7971 Gly Leu Ile Ala Ala Val Pro Phe Val Ala Glu Ile Asp Asn Leu Leu
7972          915          920          925
7975 Glu Ser Gln Lys Ala Asp Met Arg Ile Lys Ile Lys Tyr Pro Asp Gln
7976          930          935          940

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Input Set : N:\SMITH\PTO.TS.txt

Output Set: N:\CRF4\01312006\J527571.raw

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7979 His Met His Thr Val Val Pro Lys Gln Ser Asp Phe Lys Pro Ile Met
7980 945                      950                      955                      960
7983 Thr Glu Gln Gly Glu His Lys Thr Asn Val Arg Leu Arg Thr Thr Ile
7984                      965                      970                      975
7987 Leu Leu Ser His Ser Val Trp Thr Glu Ser Ser Leu Val Glu Ile Gln
7988                      980                      985                      990
7991 Leu Cys Leu Ala Val Arg Pro Gly Ser Glu Leu Glu Leu Cys Lys Pro
7992                      995                      1000                      1005
7995 Ala Lys Val Leu Phe Ala Pro Lys Pro Val Arg Arg Gly Ile
E--> 7996      1010      1015      1015      1020      1020
7999 <210> SEQ ID NO: 62
8000 <211> LENGTH: 780 → found 774
8001 <212> TYPE: DNA
8002 <213> ORGANISM: Drosophila melanogaster
8004 <220> FEATURE:
8005 <221> NAME/KEY: CDS
8006 <222> LOCATION: (1)..(780)
8007 <223> OTHER INFORMATION: CT7760
8010 <400> SEQUENCE: 62
8011 atg acc aca gca gcg cgt ccg acc ttc gat cca gcc cgc gga gga tcc      48
8012 Met Thr Thr Ala Ala Arg Pro Thr Phe Asp Pro Ala Arg Gly Gly Ser
8013 1                      5                      10                      15
8015 ggt cgc ggc gaa aag gat ctg agt gca ctg agc aag cag tac tcc agt      96
8016 Gly Arg Gly Glu Lys Asp Leu Ser Ala Leu Ser Lys Gln Tyr Ser Ser
8017                      20                      25                      30
8019 cgc gat ttg cca ggc cac acg aaa ctg aaa tac agg gag act ggc cag      144
8020 Arg Asp Leu Pro Gly His Thr Lys Leu Lys Tyr Arg Glu Thr Gly Gln
8021                      35                      40                      45
8023 ggc acc agc gat gag aac cgc aac cgt gac ttc cgc aag gag ctg gag      192
8024 Gly Thr Ser Asp Glu Asn Arg Asn Arg Asp Phe Arg Lys Glu Leu Glu
8025                      50                      55                      60
8027 gag cgc gaa cgt gag gcg cgc tcc gga acg gga gcc act tcg tcg tcg      240
8028 Glu Arg Glu Arg Glu Ala Arg Ser Gly Thr Gly Ala Thr Ser Ser Ser
8029 65                      70                      75                      80
8031 tcg ggc aag gca ctg ccc tcc att gta cgc aag gcg att gag gcg aac      288
8032 Ser Gly Lys Ala Leu Pro Ser Ile Val Arg Lys Ala Ile Glu Ala Asn
8033                      85                      90                      95
8035 aac gcc ggc ggt ggc agc agt gcc gca aag cgt tcc aag ccg gac gca      336
8036 Asn Ala Gly Gly Gly Ser Ser Ala Ala Lys Arg Ser Lys Pro Asp Ala
8037                      100                      105                      110
8039 ggg cag cag caa gcg cag cag gcg gct cag cag cag gcc gcc aat atg      384
8040 Gly Gln Gln Gln Ala Gln Gln Ala Ala Gln Gln Gln Ala Ala Asn Met
8041                      115                      120                      125
E--> 8043 gac gcc gat gag ccg ctg gac aac gat agc tcc gac agc gat      432 → 426
8044 Asp Ala Asp Glu Pro Leu Asp Asn Asp Ser Ser Asp Ser Asp
8045                      130                      135                      140
E--> 8047 tcc gat gac gat gat gcc gcc ctg ctg gcc gag ctg cag aag atc aag      480 → 474
8048 Ser Asp Asp Asp Asp Ala Ala Leu Leu Ala Glu Leu Gln Lys Ile Lys
8049 145                      150                      155                      160

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Input Set : N:\SMITH\PTO.TS.txt

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E--> 8051 cag gaa cgt ctg cag gag acg gcg cgt cgc gag tcg gaa aag aag cag
      8052 Gln Glu Arg Leu Gln Glu Thr Ala Arg Arg Glu Ser Glu Lys Lys Gln
      8053                               165                               170                               175
E--> 8055 gag gac gaa cgc ata cgc atg gag aac atc ctg tcc ggc aat cca ctg
      8056 Glu Asp Glu Arg Ile Arg Met Glu Asn Ile Leu Ser Gly Asn Pro Leu
      8057                               180                               185                               190
E--> 8059 atg aac tat gag ccc ggc acc gcc gcc tcg gca gcg gga cgt gcc tct
      8060 Met Asn Tyr Glu Pro Gly Thr Ala Ala Ser Ala Ala Gly Arg Ala Ser
      8061                               195                               200                               205
E--> 8063 gga ctg ggc ggt gat cta aag ata aag cgc cgc tgg gac gat gat gtg
      8064 Gly Leu Gly Gly Asp Leu Lys Ile Lys Arg Arg Trp Asp Asp Asp Val
      8065                               210                               215                               220
E--> 8067 gtc ttt aag aat tgc gcc aga tct gcg ccc gat aag aag acg cac ttc
      8068 Val Phe Lys Asn Cys Ala Arg Ser Ala Pro Asp Lys Lys Thr His Phe
      8069 225                               230                               235                               240
E--> 8071 gtc aat gac gcc ctg cgc tcc gat ttc cac aag aag ttc atg gac aag
      8072 Val Asn Asp Ala Leu Arg Ser Asp Phe His Lys Lys Phe Met Asp Lys
      8073                               245                               250                               255
E--> 8075 tac att aag taa
E--> 8076 Tyr Ile Lys
50813 <210> SEQ ID NO: 299
50814 <211> LENGTH: 522
50815 <212> TYPE: PRT
50816 <213> ORGANISM: Drosophila melanogaster
50818 <400> SEQUENCE: 299
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50821 1                               5                               10                               15
50824 Asp Leu Val Arg Gln Leu Lys Ala Ala Lys Glu Ser Lys Glu Lys Ile
50825                               20                               25                               30
50828 Asp Glu Glu Val Ala Arg Leu Leu Ala Leu Lys Ala Thr Leu Gly Gly
50829                               35                               40                               45
50832 Asp Ala Ala Pro Thr Asn Gln Lys Phe Thr Leu Lys Thr Pro Lys Gly
50833                               50                               55                               60
50836 Thr Arg Asp Tyr Gly Pro Gln Gln Met Thr Leu Arg Gln Gly Val Leu
50837 65                               70                               75                               80
50840 Asp Lys Ile Val Gln Val Phe Lys Arg His Gly Gly Glu Ala Ile Asp
50841                               85                               90                               95
50844 Thr Pro Val Phe Glu Leu Lys Glu Val Leu Thr Gly Lys Tyr Gly Glu
50845                               100                              105                              110
50848 Asp Ser Lys Leu Ile Tyr Asp Leu Lys Asp Gln Gly Gly Glu Ile Leu
50849                               115                              120                              125
50852 Ser Met Arg Tyr Asp Leu Thr Val Pro Leu Ala Arg Tyr Leu Ala Met
50853                               130                              135                              140
50856 Asn Lys Ile Ser Ser Ile Lys Arg Tyr His Ile Ala Lys Val Tyr Arg
50857 145                               150                              155                              160
50860 Arg Asp Asn Pro Ala Met Thr Lys Gly Arg Tyr Arg Glu Phe Tyr Gln
50861                               165                              170                              175
50864 Cys Asp Phe Asp Ile Ala Gly Thr Tyr Asp Pro Met Leu Pro Asp Ala
50865                               180                              185                              190

```

(528) 522

(576) 570

(624) 618

(672) 666

(720) 714

(768) 762

(780) 774

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/527,571

DATE: 01/31/2006

TIME: 15:59:59

Input Set : N:\SMITH\PTO.TS.txt

Output Set: N:\CRF4\01312006\J527571.raw

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50868 Glu Cys Val Lys Ile Val Ser Glu Ile Leu Asp Thr Leu Asp Ile Gly
50869      195      200      205
50872 Asp Tyr Val Ile Lys Leu Asn His Arg Gln Leu Leu Asp Gly Met Phe
50873      210      215      220
50876 Gln Ala Cys Gly Val Pro Ala Asp Ser Phe Arg Thr Ile Cys Ser Ala
50877 225      230      235      240
50880 Val Asp Lys Leu Asp Lys Ser Pro Trp Ala Asp Val Arg Lys Glu Met
50881      245      250      255
50884 Val Asp Glu Lys Gly Leu Asp Glu Ala Ala Asp Arg Ile Gly Glu
50885      260      265      270
50888 Tyr Val Arg Leu Ser Gly Gly Ala Glu Leu Val Glu Gln Leu Leu Ala
50889      275      280      285
50892 Asn Glu Lys Leu Lys Ala Val Pro Asn Ala Val Lys Gly Leu Glu Gly
50893      290      295      300
50896 Met Lys Gln Leu Leu Lys Tyr Cys Ser Ile Phe Gly Leu Asp Lys Arg
50897 305      310      315      320
50900 Val Ser Phe Asp Leu Ser Leu Ala Arg Gly Leu Asp Tyr Tyr Thr Gly
50901      325      330      335
50904 Val Ile Tyr Glu Gly Val Leu Lys Gly Glu Ser Ala Thr Val Ala Ser
50905      340      345      350
50908 Pro Ala Lys Thr Ser Gln Gln Asn Gly Glu Gln Ala Asn Glu Pro Ala
50909      355      360      365
50912 Thr Val Gly Ser Val Ala Gly Gly Gly Arg Tyr Asp Asn Leu Val Gly
50913      370      375      380
50916 Met Phe Asp Pro Arg Gly Lys Ala Val Pro Cys Val Gly Val Ser Ile
50917 385      390      395      400
50920 Gly Val Glu Arg Ile Phe Ser Val Leu Glu Ala Arg Ala Ala Ser
50921      405      410      415
50924 Gly Leu Lys Leu Arg Thr Ser Asp Val Glu Val Tyr Val Ala Ser Ala
50925      420      425      430
50928 His Lys Gly Leu His Glu Gln Arg Leu Lys Val Leu Asn Leu Leu Trp
50929      435      440      445
50932 Asp Ala Gly Val Lys Ala Glu His Ser Tyr Lys Leu Asn Pro Lys Leu
50933      450      455      460
50936 Leu Val Gln Leu Gln His Cys Glu Glu His Gln Ile Pro Leu Val Val
50937 465      470      475      480
50940 Val Leu Gly Asp Ala Glu Leu Ala Gln Gly Leu Val Lys Leu Arg Glu
50941      485      490      495
50944 Val Thr Thr Arg Glu Glu Thr Asn Val Lys Leu Glu Asp Leu Ala Ala
50945      500      505      510

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E--> 50948 CT19850 Glu Ile Arg Arg Arg Gln Gln Ala Ser Ala

E--> 50949 515 515 520 520

↓  
Pls delete



## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/527,571

DATE: 01/31/2006

TIME: 16:00:01

Input Set : N:\SMITH\PTO.TS.txt

Output Set: N:\CRF4\01312006\J527571.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:191 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
L:6917 M:280 W: Numeric Identifier already exists, Length not replaced.  
L:7023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:1248.  
L:7195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:400  
L:7996 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:61  
L:8043 M:254 E: No. of Bases conflict, LENGTH:Input:432 Counted:426 SEQ:62  
M:254 Repeated in SeqNo=62  
L:8076 M:252 E: No. of Seq. differs, <211> LENGTH:Input:780 Found:774 SEQ:62  
L:27070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:180 after pos.:1680  
M:341 Repeated in SeqNo=180  
L:27247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:181 after pos.:544  
M:341 Repeated in SeqNo=181  
L:33756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:204 after pos.:2976  
M:341 Repeated in SeqNo=204  
L:34026 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:205 after pos.:992  
L:50948 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:50948 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
L:50949 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:299  
L:50963 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:300,Line#:50960